



# Blast 2 Sequences results

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OMIM

Taxonomy

Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

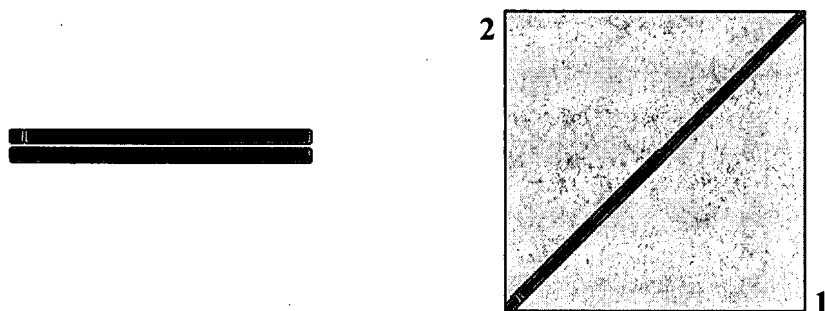
x\_dropoff: 50 expect: 10.0000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation

Sequence 1: lcl|1\_seq\_1  
Length = 1203 (1 .. 1203)

Sequence 2: lcl|2\_seq\_2  
Length = 1205 (1 .. 1205)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2072 bits (5368), Expect = 0.0  
Identities = 1133/1205 (94%), Positives = 1161/1205 (96%), Gaps = 2/1205 (0%)

Query	1	MGNLKSVAQEXXXXXXXXXXXXXXXXXXKQGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXT	60
		MGNLKS SV QEPGPPCGLGGLGLGLGCGKQGPA+PAPEPSRAPA P AP+HSP + T	
Sbjct	1	MGNLKS SV QEPGPPCGLGGLGLGLGCGKQGPASPAPEPSRAPAPATPHAPDHSPAPNSPT	60
Query	61	--QPPEGPKFPRVKNWEVGSITYDTLSAQAAQDGPCTPRRCLGSLVFPRKLQGRPSGPP	118
		+PPEGPKFPRVKNWE+GSITYDTL AQ+QDGPCTPR CLGSLV PRKLQ RPSPGPP	
Sbjct	61	LTRPPEGPKFPRVKNWELGSITYDTLCAQSQQDGPCTPRCCLGSLVLPRLQTRPSGPP	120
Query	119	APEQLLSQARDFINQYYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAW	178
		EQLLSQARDFINQYYSSIKRSGSQAHE+RLQEVEAEVA+TGTY LRESELVFGAKQAW	
Sbjct	121	PAEQLLSQARDFINQYYSSIKRSGSQAHEERLQEVEAEVASTGTYHLRESELVFGAKQAW	180
Query	179	RNAPRCVGRIQWGKLQVFDARDCRSAQEMFTYICNHIKYATNRGNLRS AITVFPQRC PGR	238
		RNAPRCVGRIQWGKLQVFDARDC SAQEMFTYICNHIKYATNRGNLRS AITVFPQ RGR	
Sbjct	181	RNAPRCVGRIQWGKLQVFDARDCSSAQEMFTYICNHIKYATNRGNLRS AITVFPQ RAPGR	240

Query	239	GDFRIWNSQLVRYAGYRQODGSGVRGDPANVEITELCIQHWTPGNRFDVLP LLLQAXXX	298
Sbjct	241	GDFRIWNSQLVRYAGYRQODGSGVRGDPANVEITELCIQHWTPGNRFDVLP LLLQAPDE	300
Query	299	XXXXXXXXXXXXXXXXXXXXXXXXXWFAALGLRWYALPAVSNM LLEIGGLEFP AAPFSGWYM	358
Sbjct	301	PELF+LPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNM LLEIGGLEF AAPFSGWYM	360
Query	359	STEIGTRNLCDPHRYNILEDVAVCM DLDTRTTSSLWKDKAAVEIN VAVLHSYQLAKVTIV	418
Sbjct	361	STEIGTRNLCDPHRYNILEDVAVCM DLDTRTTSSLWKDKAAVEIN+AVLHS+QLAKVTIV	420
Query	419	DHHAATASF MKHLENEQKARGGCPADWAWIVPPISGSLTPVFHQEMVNYFLSPA FRYQPD	478
Sbjct	421	DHHAAT SFMKHL+NEQKARGGCPADWAWIVPPISGSLTPVFHQEMVNY LSPA FRYQPD	480
Query	479	PWKGSAAKGTGITRKKTFKEVANAVKISASLMGTVM AKRVKATILYGSETGRAQSYAQQL	538
Sbjct	481	PWKGSA KG GITRKKTFKEVANAVKISASLMGT+MAKRVKATILY SETGRAQSYAQQL	540
Query	539	GRLFRKA F D P R V L C M D E Y D V V S L E H E T L V L V V T S T F G N G D P P E N G E S F A A A L M E M S G P Y N	598
Sbjct	541	GRLFRKA F D P R V L C M D E Y D V V S L E H E L V L V V T S T F G N G D P P E N G E S F A A A L M E M S G P Y N	600
Query	599	SSPRPEQH K S Y K I R F N S I S C S D P L V S S W R R K R K E S S N T D S A G A L G T L R F C V F G L G S R A Y P	658
Sbjct	601	SSPRPEQH K S Y K I R F N S + S C S D P L V S S W R R K R K E S S N T D S A G A L G T L R F C V F G L G S R A Y P	660
Query	659	HFCAFA R A V D T X X X X X X X X X X X X X X X X C G Q E E A F R G W A Q A A F Q A A C E T F C V G E D A K A	718
Sbjct	661	HFCAFA R A V D T R L E E L G G E R L L Q L G Q G D E L C G Q E E A F R G W A + A A F Q A + C E T F C V G E + A K A	720
Query	719	AARDIFSPKRSWK R Q R Y R L S A Q A E G L Q L L P G L I H V H R R K M F Q A T I R S V E N L Q S S K S T R A T	778
Sbjct	721	AA+DIFSPKRSWK R Q R Y R L S Q A E G L Q L L P G L I H V H R R K M F Q A T + S V E N L Q S S K S T R A T	780
Query	779	ILVRLDTGGQEG L Q Y Q P G D H I G V C P P N R P G L V E A L L S R V E D P P A P T E P V A V E Q L E K G S P G	838
Sbjct	781	ILVRLDT GQEG L Q Y Q P G D H I G + C P P N R P G L V E A L L S R V E D P P P T E V A V E Q L E K G S P G	840
Query	839	GPPPGWVRD P R L P P C T L R Q A L T F F L D I T X X X X X X X X X X X X X X X X A E E P R E Q Q E L E A L S Q D P R	898
Sbjct	841	GPPP WVRD P R L P P C T L R Q A L T F F L D I T S P P S P + L L R L L S T L A E E P E Q Q E L E L S Q D P R	900
Query	899	RYEEWKWFR C P T L L E V L E Q F P S V X X X X X X X X X X X X X X X X R Y Y S V S S A P S T H P G E I H L T V A	958
Sbjct	901	RYEEWKWFR C P T L L E V L E Q F P S V A L P A P L L L T Q L P L L Q P R Y Y S V S S A P + H P G E + H L T V A	960
Query	959	VLAYRTQDGLG P L H Y G V C S T W L S Q L K P G D P V P C F I R G A P S F R L P P D P S L P C I L V G P G T G I	1018
Sbjct	961	VLAYRTQDGLG P L H Y G V C S T W L S Q L K G D P V P C F I R G A P S F R L P P D P + P C I L V G P G T G I	1020
Query	1019	APFRGFWQER L H D I E S K G L Q P T M T L V F G C R C S Q L D H L Y R D E V Q N A Q Q R G V F G R V L T A F S	1078
Sbjct	1021	APFRGFWQER L H D I E S K G L Q P A P M T L V F G C R C S Q L D H L Y R D E V Q D A Q E R G V F G R V L T A F S	1080
Query	1079	REP D N P K T Y V Q D I L R T E L A A E V H R V L C L E R G H M F V C G D V T M A T N V L Q T V Q R I L A T E G D M E	1138
Sbjct	1081	REP D + P K T Y V Q D I L R T E L A A E V H R V L C L E R G H M F V C G D V T M A T + V L Q T V Q R I L A T E G D M E	1140

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Query 1139 LDEAGDVIGVLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERQLRGAVPWAFDPPGS 1198
          LDEAGDVIGVLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQER LRGAVPWAFDPPG
Sbjct 1141 LDEAGDVIGVLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERHLRGAVPWAFDPPGP 1200

Query 1199 DTNSP 1203
          DT P
Sbjct 1201 DTPGP 1205
```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H  
0.320 0.135 0.423

#### Gapped

Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 10,229

Number of extensions: 6074

Number of successful extensions: 6

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1203

Length of database: 1,610,148,966

Length adjustment: 147

Effective length of query: 1056

Effective length of database: 1,610,148,819

Effective search space: 1700317152864

Effective search space used: 1700317152864

Neighboring words threshold: 9

X1: 16 ( 7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 85 (37.4 bits)